Figure 2

```
 M    A    V    L    G    L    L    F    C    L    V    T    F    P    S    C
ATG  GCT  GTC  TTG  GGG  CTG  CTC  TTC  TGC  CTG  GTG  ACA  TTC  CCA  AGC  TGT
 V    L    S
GTC  CTG  TCC    (-1 to -19, Leader)

 Q    V    Q    V    K    E    S    G    P    F    L    V    P    P    S    Q
CAG  GTG  CAG  GTG  AAG  GAG  TCA  GGA  CCT  TTC  CTG  GTG  CCC  CCC  TCA  CAG
 S    L    S    I    T    C    T    V    S    G    F    S    L    T
AGC  CTG  TCC  ATC  ACA  TGC  ACT  GTC  TCA  GGG  TTC  TCA  TTA  ACC
  (1-30, Frame work 1)

 T    Y    G    V    S
ACC  TAT  GGT  GTA  AGC    (31-35, CDR 1)

 W    I    R    Q    P    P    G    K    G    L    E    W    L    G
TGG  ATT  CGC  CAG  CCT  CCA  GGA  AAG  GGT  CTG  GAG  TGG  CTG  GGA
  (36-49, Frame work 2)

 A    I    W    G    D    G    T    T    N    Y    H    S    A    L    I    S
GCA  ATT  TGG  GGT  GAC  GGG  ACC  ACA  AAT  TAT  CAT  TCA  GCT  CTC  ATA  TCC
  (50-65, CDR 2)

 R    L    S    I    S    K    D    N    S    K    S    Q    V    F    L    K
AGA  CTG  AGC  ATC  AGC  AAG  GAT  AAC  TCC  AAG  AGC  CAA  GTT  TTC  TTA  AAA
 L    N    S    L    Q    T    D    D    T    A    T    Y    Y    C    A    K
CTG  AAC  AGT  CTG  CAA  ACT  GAT  GAC  ACG  GCC  ACG  TAC  TAC  TGT  GCC  AAA
  (66-97, Frame work 3)

 L    G    N    Y    D    A    L    D   *W   Y
CTG  GGT  AAC  TAC  GAT  GCT  CTG  GAC  TAC
  (98-106, CDR 3)

 W    G    Q    G    T    S    V    T    V    S    S
TGG  GGT  CAA  GGA  ACC  TCA  GTC  ACC  GTC  TCC  TCA
  ( 107-117, Frame work 4)

 A    K    T    T    P    P    P    V    Y    P    L    V    P    G    S    L
GCC  AAA  ACG  ACA  CCC  CCA  CCC  GTC  TAT  CCA  TTG  GTC  CCT  GGA  AGC  TTG  GG
  (Constant region)
```

Figure 3(B)

```
1A7:    1  QVQVKESGPFLVPPSQSLSITCTVSGFSLTTYGVSWIRQPPGKGLEWLGAIWGDGTTNYH   60

1       1          .G..A.................S....V...........V.....S....   52
2       1  ...LQ...G..A.................S..IT.V...........V:....N.:..   60
3      20  ...L....G..A.................G...N.V...........T...N.S.D.N   79
4       1  ...L..T..G..A.................S...H.V.........VV..S...S...N   60
5       1  ...L....G..A.................S...H.V..........V..AG.S...N   60
6       1  ...L....G..A.................S...H.V..........V..AG.S...N   60
7       1  ...L....G..A..............P..S...D.V..........V...G.S...N   60
8      23  ...LQ...G..A.................G...N.V...........M.....N.D.N   82
9       1  ...L....G..A.................G...N.V...........M.....N.D.N   60
10    133  ...LQ...G..A.................G...N.V...........M.....N.D.N  192
11     20  ...L....G..A.................G...N.V...........M.....N.D.N   79
12      1  ...L....G..A...............SR.S.H.V...........H...G.N.D.N   60
13     21  .HL....V..A.................N...H.V...........V..AG.N...N   80
14     23  ...LQ...G..A.................G...N.V...........M.....N.D.N   82
15      1  ...LQ...G..A.................G...N.V...........M.....N.D.N   60

                                                          DYWG
1A7:   61  SALISRLSISKDNSKSQVFLKLNSLQTDDTATYYCAKL--------GNYDALDYWQGTSVTVSS  117

1      53  ..............................P-----YDYExxxxx[FV]...TL..  109
2      61  ..........................x-----xxxxxxx.KE]  120
3      80  .T.K...T.T..........M........R....SVSIYYYGRSDK.FT.E]  144
4      61  ..K.................M........M...Rx------xx.D.Y.ME]  119
5      61  ..M.................M........M...Rx---xxxxxx.Y.ME]  120
6      61  ..M.................M........M...Rx------xxxx.Y.ME]  118
7      61  ..M.................M...X....M...xx----xxx.X.Y.ME]  119
8      83  ..K.................M..H.....R...RE------=RDYR.[FV]...T....  138
9      61  ..K.................M..H.....R...RE------=RDYR.[FV]...TL...  116
10    193  ..K.................M..H.....R...RE------=RDYR.[FV]...T....  248
11     80  ..K.................M..H.....R...RE------=RDYR.[FV]...TL...  135
12     61  ..K.................M........RD------GYYDx.M[FV]  117
13     81  ..M.................M...I...I....x-----xxxxx.Y.ME]  139
14     83  ..K.................M..H.....R...RE------=RDYR.[FV]...T....  138
15     61  ..K.................M..H.....R...RE------=RDYR.[FV]...T....  116
```

Figure 3(C)

```
                                   ****************           ******
VL consensus:   1  DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRF   60
1A7:            1  .............................................P....N..........   60


                   *                          *********
VL consensus:  61  SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK           112
1A7:           61  ...........................................................    112




                                      *****            **********
VH consensus:   1  QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWGDGSTNYN   60
1A7:            1  ...V.....F..P................T...S.I............A.....T...H   60


                   *****                        ***********
VH consensus:  61  SALKSRLSISKDNSKSQVFLKMNSLQTDDTARYYCARExxxxYYAMDYWGQGTSVTVSS   119
1A7:           61  ...I................L.........T...KL--GN.D.SH..........   117
```